

- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kawamura, Yukio; Morita, Akihiro; Izumo, Koji.; Saka, Tomohide.
- (ii) TITLE OF INVENTION: ANTITUMOR PROTEIN AND GENE ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 (B) STREET: 345 PARK AVENUE
 (C) CITY: NEW YORK
 (D) STATE: NEW YORK
 (E) COUNTRY: USA
 (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: FLOPPY DISK
 (B) COMPUTER: IBM PC COMPATIBLE
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: MICROSOFT WORD 97
- (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: 09/023,731
 (B) FILING DATE: 13-FEB-1998
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: JP 29275/1997
 (B) FILING DATE: 13-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: KENNETH H. SONNENFELD
 (B) REGISTRATION NUMBER: 33,285
 (C) REFERENCE/DOCKET NUMBER: 3479-4000
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (212) 758-4800
 (B) TELEFAX: (212) 751-6849
 (C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Pro Ile Arg Leu Ser Iys Glu Lys Ile Asn Asp Leu Leu Gln Arg
 1 5 10 15

473997_1

- 2 -

```

Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr
      20      25      30
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg
      35      40      45
His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile
      50      55      60
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile
      65      70      75      80
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala
      85      90      95
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
      100      105      110
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu
      115      120      125
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro
      130      135      140
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr
      145      150      155      160
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val
      165      170      175
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu
      180      185      190
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val
      195      200      205
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr
      210      215      220
Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr
      225      230      235      240
Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg
      245      250      255
Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu
      260      265      270
Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr
      275      280      285
Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly
      290      295      300
Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr
      305      310      315      320
Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile
      325      330      335
Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe
      340      345      350
Ala Ala Lys Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu
      355      360      365
Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr
      370      375      380
Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr
      385      390      395      400
Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg
      405      410      415
Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly
      420      425      430
Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr
      435      440      445
Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly
      450      455      460

```

473997_1

- 3 -

```

Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met
465          470          475          480
Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly
          485          490          495
Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln
          500          505          510
Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu
          515          520          525
Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro
          530          535          540
Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val
545          550          555          560
Asn Tyr Leu Gly Val Ser *
          565

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1701
- (B) TYPE: nucleic acid
- (C) TOPOLOGY: linear
- (D) STRANDNESS: Single

(ii) MOLECULE TYPE: cDNA to RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

ATG CCG ATA CGT CTT TCC AAA GAA AAA ATC AAC GAC CTG CTG CAA CGT      48
Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg
   1              5              10              15

TCT CAA GGG GAT CTT ACT TCC TCG CAA CAC GAA ATT GTA CAT TTC ACT      96
Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr
   20              25              30

GAT GTT TTC ATT GCT GGC AGT GGT CCC ATT AGC TGT ACT TAC GCC CGC     144
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg
   35              40              45

CAC ATC ATT GAC AAT ACC TCA ACT ACA AAG GTT TAC ATG GCC GAA ATA     192
His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile
   50              55              60

GGT TCT CAA GAT AAC CCT GTC ATC GGG GCC CAT CAC AAG AAC TCC ATA     240
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile
   65              70              75              80

AAG TTT CAG AAA GAC ATT GAC AAG TTT GTG AAT ATC ATC AAC GGT GCC     288
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala
   85              90              95

CTC CAG CCG ATT TCG ATT TCG CCA TCG GAC ACC TAC CAG CCC ACT CTC     336
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
  100              105              110

```

473997_1

- 4 -

GCT GTA GCA GCG TGG GCG CCG CCC ATC GAT CCT GCC GAA GGC CAG CTC	384
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu	
115 120 125	
GTG ATT ATG GGA CAC AAT CCG AAT CAG GAG GCC GGC CTG AAC CTT CCC	432
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro	
130 135 140	
GGT AGC GCT GTC ACT AGG ACA GTC GGG GGG ATG GCG ACC CAC TGG ACT	480
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr	
145 150 155 160	
TGC GCG TGT CCT ACT CCA CAT GAC GAA GAG AGG GTC AAC AAC CCA GTT	528
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val	
165 170 175	
GAC AAG CAG GAG TTC GAC GCA CTG CTC GAA CGT GCT AAA ACA TTG CTC	576
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu	
180 185 190	
AAC GTT CAC AGC GAC CAG TAC GAC GAT TCT ATC CGT CAG ATA GTT GTC	624
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val	
195 200 205	
AAA GAG ACT CTT CAG CAG ACC CTT GAT GCG TCG CGG GGT GTG ACC ACT	672
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr	
210 215 220	
CTC CCG CTG GGG GTG GAG CGC CGT ACG GAC AAT CCT ATT TAT GTC ACC	720
Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr	
225 230 235 240	
TGG ACC GGT GCC GAT ACC GTC CTT GGT GAT GTG CCG AAG AGT CCC CGA	768
Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg	
245 250 255	
TTC GCT TTG GTT ACA GAG ACG AGA GTG ACG AAG CTT ATT GTC AGT GAA	816
Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu	
260 265 270	
ACC AAT CCG ACG CAG GTT GTT GCT GCG TTG CTA CGT AAC TTG AAT ACA	864
Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr	
275 280 285	
AGC AAC GAT GAA CTT GTC GTG GCC AAG AGT TTC GTC ATA GCT TGT GGA	912
Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly	
290 295 300	
GCA GTC TGC ACA CCG CAA ATC TTG TGG AAC AGC AAC ATC CGC CCA TAT	960
Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr	
305 310 315 320	
GCG CTT GGT CGC TAC CTC AGC GAA CAG TCC ATG ACT TTT TGT CAG ATC	1008
Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile	
325 330 335	

473997_1

- 5 -

GTT CTC AAG AGG GGC ATA GTC GAT GCC ATC GCT ACT GAC CCT CGC TTC	1056
Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe	
340 345 350	
GCT GCG AAG GTT GAG GCG CAC AAG AAG AAG CAC CCC GAT GAC GTG CTG	1104
Ala Ala Lys Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu	
355 360 365	
CCC ATT CCA TTC CAC GAG CCT GAA CCT CAA GTG ATG ATT CCG TAC ACG	1152
Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr	
370 375 380	
TCG GAC TTC CCT TGG CAT GTT CAG GTG CAT CGC GAT GCA TTC TCA TAT	1200
Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr	
385 390 395 400	
GGT GAT GTT GGA CCC AAG GCC GAC CCG CGT GTT GTC GTC GAT CTG AGG	1248
Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg	
405 410 415	
TTT TTC GGC AAA TCA GAT ATT GTC GAA GAA AAT CGA GTG ACT TTC GGT	1296
Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly	
420 425 430	
CCG AAC CCT AAG CTA CGC GAG TGG GAA GCG GGT GTT ACA GAC ACT TAT	1344
Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr	
435 440 445	
GGA ATG CCA CAG CCG ACA TTC CAT GTC AAG CCG ACC AAC GCC GAT GGA	1392
Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly	
450 455 460	
GAC CGT GAC CAG AGG ATG ATG AAT GAT ATG ACC AAC GTC GCG AAC ATG	1440
Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met	
465 470 475 480	
CTG GGT GGG TAC CTT CCT GGC TCC TAC CCT CAA TTT ATG GCA CCT GGT	1488
Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly	
485 490 495	
CTC GTA CTG CAC ATC ACG GGA ACT ACT CGG ATC GGG ACA GAT GAT CAA	1536
Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln	
500 505 510	
ACT TCT GTT GCT GAT CCG ACA TCA AAG GTT CAT AAC TTC AAC AAT CTG	1584
Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu	
515 520 525	
TGG GTC GGC GGG AAT GGG TGC ATT CCA GAT GCG ACT GCC TGC AAC CCG	1632
Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro	
530 535 540	
ACT CGT ACG AGC GTC GCG TAT GCG CTC AAG GGT GCT GAG GCT GTA GTC	1680
Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val	
545 550 555 560	

473997_1

- 6 -

AAT TAC CTT GGC GTC TCC TGA
Asn Tyr Leu Gly Val Ser *
565

1701

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser
1 5 10 15
Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His
20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser
1 5 10 15
Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr Asp
20 25 30
Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg His
35 40 45
Ile Ile Asp Asn Thr Ser Thr Thr Lys
50 55

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Tyr Met Ala Glu Ile Gly Ser Gln Asp Asn Pro Val Ile Gly Ala
1 5 10 15
His His Lys

473997_1

- 7 -

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Phe Val Asn Ile Ile Asn Gly Ala Leu Gln Pro Ile Ser Ile Ser Pro
 1           5           10           15
Ser Asp Thr Tyr Gln Pro Thr Leu Ala Val Ala Ala Trp Ala Pro Pro
 20           25           30
Ile Asp Pro Ala Glu Gly Gln Leu Val Ile Met Gly His Asn Pro Asn
 35           40           45
Gln Glu Ala Gly Leu Asn Leu Pro Gly Ser Ala Val Thr
 50           55           60
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Arg Thr Val Gly Gly Met Ala Thr His Trp Thr Cys Ala Cys Pro Thr
 1           5           10           15
Pro His Asp Glu Glu Arg Val Asn Asn Pro Val Asp Lys
 20           25
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu Asn Val
 1           5           10           15
His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val Lys
 20           25           30
```

(2) INFORMATION FOR SEQ ID NO:9:

473997_1

- 8 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu	Thr	Leu	Gln	Gln	Thr	Leu	Asp	Ala	Ser	Arg	Gly	Val	Thr	Thr	Leu
1				5					10					15	
Pro	Leu	Gly	Val	Glu	Arg	Arg	Thr	Asp	Asn	Pro	Ile	Tyr	Val	Thr	Trp
			20					25					30		
Thr	Gly	Ala	Asp	Thr	Val	Leu	Gly	Asp	Val	Pro	Lys	Ser	Pro	Arg	Phe
		35					40					45			
Ala	Leu	Val	Thr	Glu	Thr	Arg	Val	Thr	Lys						
		50				55									

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu	Ile	Val	Ser	Glu	Thr	Asn	Pro	Thr	Gln	Val	Val	Ala	Ala	Leu	Leu
1				5				10						15	
Arg	Asn	Leu	Asn	Thr	Ser	Asn	Asp	Glu	Leu	Val	Val	Ala	Lys		
		20						25				30			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser	Phe	Val	Ile	Ala	Cys	Gly	Ala	Val	Cys	Thr	Pro	Gln	Ile	Leu	Trp
1				5				10						15	
Asn	Ser	Asn	Ile	Arg	Pro	Tyr	Ala	Leu	Gly	Arg	Tyr	Leu	Ser	Glu	Gln
			20					25				30			
Ser	Met	Thr	Phe	Cys	Gln	Ile	Val	Leu	Lys	Arg	Gly	Ile	Val	Asp	Ala
		35					40					45			
Ile	Ala	Thr	Asp	Pro	Arg	Phe	Ala	Ala	Lys						
		50				55									

473997_1

- 9 -

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val	Glu	Ala	His	Lys	Lys	Lys	His	Pro	Asp	Asp	Val	Leu	Pro	Ile	Pro
1				5					10					15	
Phe	His	Glu	Pro	Glu	Pro	Gln	Val	Met	Ile	Pro	Tyr	Thr	Ser	Asp	Phe
			20					25					30		
Pro	Trp	His	Val	Gln	Val	His	Arg	Asp	Ala	Phe	Ser	Tyr	Gly	Asp	Val
			35				40					45			
Gly	Pro	Lys													
			50												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Asp	Pro	Arg	Val	Val	Val	Asp	Leu	Arg	Phe	Phe	Gly	Lys	Ser	Asp
1				5					10					15	
Ile	Val	Glu	Glu	Asn	Arg	Val	Thr	Phe	Gly	Pro	Asn	Pro	Lys		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu	Arg	Glu	Trp	Glu	Ala	Gly	Val	Thr	Asp	Thr	Tyr	Gly	Met	Pro	Gln
1				5					10					15	
Pro	Thr	Phe	His	Val	Lys	Arg	Thr	Asn	Ala	Asp	Gly	Asp	Arg	Asp	Gln
			20					25				30			
Arg	Met	Met	Asn	Asp	Met	Thr	Asn	Val	Ala	Asn	Met	Leu	Gly	Gly	Tyr
			30				40					45			

473997_1

- 10 -

Leu Pro
50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly	Ser	Tyr	Pro	Gln	Phe	Met	Ala	Pro	Gly	Leu	Val	Leu	His	Ile	Thr
1				5					10					15	
Gly	Thr	Thr	Arg	Ile	Gly	Thr	Asp	Asp	Gln	Thr	Ser	Val	Ala	Asp	Pro
			20				25					30			
Thr	Ser	Lys													
		35													

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val	His	Asn	Phe	Asn	Asn	Leu	Trp	Val	Gly	Gly	Asn	Gly	Cys	Ile	Pro
1				5					10					15	
Asp	Ala	Thr	Ala	Cys	Asn	Pro	Thr	Arg	Thr	Ser	Val	Ala	Tyr	Ala	Leu
			20				25					30			
Lys															

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly	Ala	Glu	Ala	Val	Val	Asn	Tyr	Leu	Gly	Val	Ser
1				5					10		

(2) INFORMATION FOR SEQ ID NO:18:

473997_1

- 11 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Ser Ile Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile
1 5 10 15
Asn Gly Ala Leu Gln Pro
20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDNESS: Single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAGAGACCAT GGGGTATCGT CTTTCC 26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: nucleic acid
(C) STRANDNESS: Single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAGAGAGGAT CCGGAGACGC CAAGGAT 27

473997_1